MRSA Surveillance Programmes Worldwide: Moving towards a harmonised international approach

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Abstract

Multinational surveillance programmes for methicillin-resistant *Staphylococcus aureus* (MRSA) are dependent on national structures for data collection. This study aimed to capture the diversity of national MRSA surveillance programmes and propose a framework for harmonisation of MRSA surveillance.

The International Society of Antimicrobial Chemotherapy (ISAC) MRSA Working Group conducted a structured survey on MRSA surveillance programmes and organised a webinar to discuss the programmes' strengths and challenges and guidelines for harmonisation.

Completed surveys represented 24 MRSA surveillance programmes in 16 countries. Several countries reported separate epidemiological and microbiological surveillance. Informing clinicians and national policymakers were the most common purposes of surveillance. Surveillance of bloodstream infections (BSI) was present in all programmes. Other invasive infections were often included. Three countries reported active surveillance of MRSA carriage. Methodology and reporting of antimicrobial susceptibility, virulence factors, molecular genotyping and epidemiological metadata varied greatly.

Current MRSA surveillance programmes rely upon heterogeneous data collection systems, which hampers international epidemiological monitoring and research. To harmonise MRSA surveillance, we suggest improving the integration of microbiological and epidemiological data, implementation of central biobanks for MRSA isolate collection, and inclusion of a representative sample of skin and soft tissue infection cases in addition to all BSI cases.

Keywords: Antimicrobial resistance, *Staphylococcus aureus*, monitoring, epidemiology

1. Introduction

Antimicrobial resistance (AMR) is one of the greatest threats to public health. Methicillin-resistant *Staphylococcus aureus* (MRSA) is the second most common cause of antibiotic-resistant bacterial infection in the European Union (EU) and European Economic Area (EEA) [1]. Many MRSA originate from a limited number of historically dominant clonal lineages [2]. While some MRSA clones are found worldwide, others are restricted to certain geographic areas, implying differences in transmission [3]. To analyse MRSA transmission and to decrease the incidence of new infections, international epidemiological research is crucial, and this research depends on MRSA surveillance programmes.

Many MRSA surveillance programmes exist worldwide, but only a few are multinational [4]. One European multinational programme is the European Antimicrobial Resistance Surveillance Network (EARS-Net) [5]. EARS-Net is coordinated by the European Centre for Disease Prevention and Control (ECDC) and depends on national surveillance systems. While susceptibility testing and interpretation recommendations have been harmonised (EUCAST) [5], national surveillance programmes use different sampling strategies and laboratory techniques that can bias analyses [6]. Also, non-European multinational MRSA surveillance programmes mostly depend on national networks using different methodologies. Examples are the Asian Network for Surveillance of Resistant Pathogens (ANSORP), the Latin American Network for Antimicrobial Resistance Surveillance (ReLAVRA), the SENTRY Antimicrobial Surveillance Program and the Tigecycline Evaluation and Surveillance Trial (T.E.S.T.), now embedded in the Antimicrobial Testing Leadership and Surveillance (ATLAS) database [7-11].

Heterogeneity in testing and sampling practices hampers international epidemiological surveillance and the establishment of an early warning system for emerging MRSA clones [4,12,13]. Additionally, it lowers the quality of available data. This can be illustrated by the experiences of the MACOTRA study group, which aimed to establish an MRSA strain collection to analyse transmission success of MRSA. However, drafted definitions of successful versus unsuccessful MRSA strains were not applicable due to the heterogeneity described above. As a result, multiple strategies for strain selection were adopted, leading to selection bias and decreased data comparability. This demonstrates that the current organisation of MRSA surveillance systems and reference laboratories are not sufficient to support a greater understanding of MRSA transmission, nor to detect emerging, virulent strains.

The aim of this project was to capture the diversity of existing national and institutional MRSA surveillance programmes and propose a framework for a standardised (inter)national surveillance network. A structured survey on current MRSA surveillance practices was conducted, followed by a

webinar organised by the International Society of Antimicrobial Chemotherapy (ISAC) MRSA Working Group.

2. Methods

ISAC MRSA Working Group members were contacted to identify directors or head microbiologists of national or regional MRSA surveillance programmes or staphylococcal reference laboratories in their respective countries. Other representatives of national organisations participating in EARS-Net were contacted directly [5]. All representatives were invited to participate in a structured survey drafted by the executive committee of the ISAC MRSA Working Group (MCV (chair), MZD, HS, VB, SS). This survey contained sections about organisational structure, surveillance goals, strain and sample characteristics, epidemiological metadata and laboratory reports. An overview of the survey is given in supplementary data.

Additionally, surveillance programme representatives were invited to participate in a webinar, held on 10 March 2021, organised by the ISAC MRSA Working Group and the MACOTRA study group, which was entitled: 'Regional and National MRSA Surveillance Programs Worldwide: Results of a Survey and Discussion of Current Practices'. Its purpose was to present an overview of surveillance programmes to an international audience, discuss these programmes' strengths and challenges, and discuss the requirements for harmonisation of MRSA surveillance.

3. Results

Representatives of 12 MRSA surveillance programmes in 9 countries were invited through the ISAC MRSA Working Group (Figure 1). Another 21 national organisations participating in EARS-Net were also invited. In total, 18 surveys were completed between January and April 2021, representing 24 MRSA surveillance programmes in 14 European and 2 non-European countries. Multiple surveillance programmes were described for Belgium (3), Germany (3), France (2), Indonesia (2), Switzerland (2) and the United States of America (USA) (2). Fourteen surveillance programmes in 8 countries were presented at the webinar.

3.1 Survey

A summary of survey results is given in Table 1.

3.1.1 Surveillance structure and purpose

All countries conducted surveillance at the national level, except Malta. In Malta, surveillance was performed at the sole tertiary hospital, but covered >90% of all national testing. In four countries, surveillance was primarily conducted at the hospital level and organised around the surveillance of

bloodstream infections (BSI). In the Czech Republic, all hospitals performed some MRSA surveillance, and MRSA BSI surveillance captured ~80% of the population. In Ireland and Poland, passive surveillance was performed through EARS-Net participation, and several national structured surveys were conducted in the past 20 years. For Indonesia, active MRSA surveillance was performed in several hospitals, but most surveillance was conducted for research purposes.

In Belgium, France and Germany, multiple separate programmes for epidemiological and microbiological surveillance were reported. In Switzerland, a local initiative focused on molecular surveillance of MRSA exists in addition to the national surveillance system, ANRESIS, which gathers epidemiological data for all antimicrobial-resistant microorganisms. In the USA, at least two large MRSA surveillance programmes exist: a national programme on MRSA BSI in which most hospitals participate and a population-based programme of invasive MRSA infections covering ~5% of the population [14].

Most surveillance programmes served multiple goals. The most common purpose of surveillance was to inform clinicians, public health workers, and laboratories about current resistance trends (17/18). Other epidemiological goals were informing national policymakers (14/18) or EARS-Net participation (for all current EU/EEA countries except Norway). Research goals included studies on staphylococcal virulence factors (12/18), resistance profiles, specific clones such as LA-MRSA, risk factor analysis, monitoring effectiveness of interventions or outbreak investigations.

3.1.2 Collection of isolates, microbiological and epidemiological data

Results of BSI isolates were collected in all surveillance programmes. Collection of wound (15/18), skin (12/18) or nose, throat or perineum (12/18) isolates also occurred frequently. Eleven programmes reported the inclusion of isolates from other clinical sample types, such as cerebrospinal fluid, urine, pus, sputum or all clinical samples (6/11). Active surveillance of MRSA carriage was reported only for Denmark, the Netherlands and Norway. Isolates from outpatients (9/18) and the general community (10/18) were also reported, but systematic active surveillance of these groups was performed only in Denmark, the Netherlands and Norway. Long-term storage of isolates varied, ranging from BSI isolates only to all submitted isolates. Programmes with an epidemiological focus often lacked routine isolate collection.

Most programmes collected microbiological data, such as antimicrobial susceptibilities (14/18) and the presence of virulence factors (11/18). The presence of the Panton-Valentine leukocidin (PVL) toxin was most commonly tested (8/11). Eleven programmes performed genotyping on all isolates, with *spa* typing as the most common method (6/11). A wide range of genotyping techniques were reported: whole genome sequencing (WGS) (10/11), *spa* typing (8/11), multilocus sequence typing

(MLST) (6/11), pulsed-field gel electrophoresis (PFGE) (3/11), *agr* group typing (Belgium), CC398 subtyping (Denmark), MLVA (Netherlands), MLVF (Poland), DNA microarray (Ireland), SCC*mec* typing (USA), CC8 subtyping (USA) and double locus sequence typing (local Swiss initiative).

Regarding epidemiological metadata, demographic variables were most commonly collected (16/18), followed by clinical information (14/18), MRSA risk factors (6/18) and outbreak metadata (4/18).

3.2 Webinar

The goals, strengths, challenges and future plans of ten MRSA surveillance programmes in eight countries were presented at the ISAC MRSA webinar. Strengths were the robust network of local laboratories and/or hospitals in the Czech Republic, France and Poland, as well as the national surveillance programmes in Belgium, Denmark, Germany, the Netherlands and Switzerland. In Denmark and the Netherlands, the strong collaboration between epidemiological and microbiological departments and existing WGS pipelines enhanced MRSA surveillance. However, limited collaboration between epidemiological and microbiological surveillance structures posed a major challenge for Belgium, France, Germany and Switzerland. The representatives of the Czech Republic, Denmark, Germany, the Netherlands, Poland and Switzerland advocated for the implementation of WGS as a default genotyping technique and an accompanying platform to share WGS data. For many surveillance programmes, stability of financial support was a concern.

Based on our results and webinar discussions, the ISAC MRSA Working Group, MRSA surveillance worldwide study group and the MACOTRA study group propose three suggestions to harmonise MRSA surveillance.

1. Inclusion of all BSI cases and a representative number of skin and soft-tissue infection (SSTI) cases in proportion to MRSA prevalence
2. Integration of microbiological and epidemiological data
3. Implementation of central biobanks at the national level for the collection and further characterisation of MRSA strains using common nomenclature allowing international comparisons

The challenges and our proposal for harmonised surveillance are summarised in Figure 2.

4. Discussion

Our study presents an overview of existing MRSA surveillance programmes in various parts of the world with an emphasis on European countries. It demonstrates the great diversity of MRSA

surveillance programmes, both in surveillance structure as well as in microbiological and epidemiological data collection. Factors potentially driving this diversity are the primary goals of surveillance, the population size, MRSA prevalence and laboratory capacity. To improve the work of these systems, a harmonised approach for surveillance programmes is needed.

We propose the inclusion of SSTI cases in addition to all BSI cases. BSI cases represent the most life-threatening MRSA infections. Because these cases are clearly defined, they provide high quality data for surveillance. Most surveillance programmes already include BSI cases.
MRSA BSIs are predominantly endogenous infections, preceded by carriage and/or non-invasive infections [15,16]. For this reason, it is desirable to include non-BSI cases in surveillance as well. SSTIs represent the majority of *S. aureus* infections and are often acquired in the community. Inclusion of SSTIs in surveillance likely increases the probability of detecting emerging clones, which may also have significant public health impact. We recommend including a representative number of SSTI cases in proportion to BSI cases and MRSA prevalence to limit selection bias. This proportion will depend on the number of estimated MRSA BSI cases within the country, considering the expected volume and thus feasibility. A clear definition of SSTI such as presented in the CDC/NHSN Patient Safety Component Manual must be used to prevent misclassification [17].

The integration of microbiological and epidemiological data should be improved to enhance data quality [4,12]. Completion of a standardised epidemiological metadata report for each submitted case is essential. In addition to demographic data (i.e., age, gender and place of residence), the sampling date and site and classification of the isolate as being from infection or colonisation are necessary. Also required is the information on relevant risk factors for MRSA acquisition to assign the patient/carrier to a defined risk group or to identify new risk factors.

The implementation of a central MRSA biobank at the national level is needed to collect isolates corresponding to the obtained epidemiological data. Typically, this biobank would be maintained by a reference laboratory, which can provide genotyping, antimicrobial susceptibility testing and testing for virulence genes on a well-defined sample of isolates. We advocate for the use of WGS as the routine genotyping technique along with common nomenclature allowing international comparisons, and incorporate detailed phylogenetic data for local, national, and international comparisons. Furthermore, we recommend repeating the structured survey undertaken by Grundmann *et al.*, to provide an update of MRSA epidemiology at the European level [18].

We advocate that professional microbiological societies support guideline development for harmonisation. Due to its focus, aims, international representation and goals, ISAC could take the lead

in this process. These guidelines should include BSI/SSTI definitions and a report template for epidemiological metadata. Additionally, a feasible ratio of BSI/SSTI cases for inclusion should be determined in collaboration with programme representatives. Furthermore, we recommend the development of an international repository for standardised surveillance data, including WGS data. Other suggestions for the harmonisation of AMR surveillance should be considered [4,12,19,20], such as the alignment of surveillance goals and standardised methodology for data collection, data analysis and data sharing.

Although many countries expend substantial effort and resources on MRSA surveillance, stability of financial support is a general concern. This should be recognised in guideline development as national health budgets will greatly influence the opportunities for harmonisation of surveillance programmes.

Inclusion bias may have limited the generalisability of our study results. Nevertheless, we were able to highlight the diversity of surveillance programmes, and our webinar enabled MRSA surveillance experts to discuss their differences directly. This guided the development of our proposal for the harmonisation of MRSA surveillance programmes.

In conclusion, current MRSA surveillance programmes rely upon heterogeneous data collection, which hampers international epidemiological monitoring and research. For harmonisation of MRSA surveillance, we suggest including SSTI cases in proportion to collected BSI cases, improving the integration of microbiological and epidemiological data, implementing central biobanks for the collection and further characterisation of MRSA isolates, and genotyping of a structured sample of these isolates, preferably using WGS.

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Declarations

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References

[1] Cassini A, Högberg LD, Plachouras D, Quattrocchi A, Hoxha A, Simonsen GS, et al. Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in the EU and the European Economic Area in 2015: a population-level modelling analysis. Lancet Infect Dis 2019;19:56–66. https://doi.org/10.1016/S1473-3099(18)30605-4.

[2] Enright MC, Robinson DA, Randle G, Feil EJ, Grundmann H, Spratt BG. The evolutionary history of methicillin-resistant Staphylococcus aureus (MRSA). Proc Natl Acad Sci 2002;99:7687–92. https://doi.org/10.1073/pnas.122108599.

[3] Stefani S, Chung DR, Lindsay JA, Friedrich AW, Kearns AM, Westh H, et al. Meticillin-resistant Staphylococcus aureus (MRSA): global epidemiology and harmonisation of typing methods. Int J Antimicrob Agents 2012;39:273–82. https://doi.org/10.1016/j.ijantimicag.2011.09.030.

[4] Diallo OO, Baron SA, Abat C, Colson P, Chaudet H, Rolain J-M. Antibiotic resistance surveillance systems: A review. J Glob Antimicrob Resist 2020;23:430–8. https://doi.org/10.1016/j.jgar.2020.10.009.

[5] European Centre for Disease Prevention and Control. Surveillance of antimicrobial resistance in Europe - Annual report of the European Antimicrobial Resistance Surveillance Network (EARS-Net) 2018. Stockholm: ECDC; 2019. https://doi.org/10.2900/22212.

[6] The European Committee on Antimicrobial Susceptibility Testing. EUCAST. https://eucast.org/ (accessed June 23, 2021).

[7] Song J-H, Hsueh P-R, Chung DR, Ko KS, Kang C-I, Peck KR, et al. Spread of methicillin-resistant Staphylococcus aureus between the community and the hospitals in Asian countries: an ANSORP study. J Antimicrob Chemother 2011;66:1061–9. https://doi.org/10.1093/jac/dkr024.

[8] Ashley EA, Recht J, Chua A, Dance D, Dhorda M, Thomas N V., et al. An inventory of supranational antimicrobial resistance surveillance networks involving low- and middle-income countries since 2000. J Antimicrob Chemother 2018;73:1737–49. https://doi.org/10.1093/jac/dky026.

[9] WHO/PAHO. Latin American Surveillance Network of Antimicrobial Resistance (ReLAVRA) https://www.paho.org/en/topics/antimicrobial-resistance/latin-american-network-antimicrobial-resistance-surveillance (accessed December 13, 2021).

[10] Diekema DJ, Pfaller MA, Shortridge D, Zervos M, Jones RN. Twenty-Year Trends in Antimicrobial Susceptibilities Among Staphylococcus aureus From the SENTRY Antimicrobial Surveillance Program. Open Forum Infect Dis 2019;6:S47–53. https://doi.org/10.1093/ofid/ofy270.

[11] Seifert H, Blondeau J, Dowzicky MJ. In vitro activity of tigecycline and comparators (2014–2016) among key WHO 'priority pathogens' and longitudinal assessment (2004–2016) of antimicrobial resistance: a report from the T.E.S.T. study. Int J Antimicrob Agents 2018;52:474–84. https://doi.org/10.1016/j.ijantimicag.2018.07.003.

[12] Tacconelli E, Sifakis F, Harbarth S, Schrijver R, van Mourik M, Voss A, et al. Surveillance for control of antimicrobial resistance. Lancet Infect Dis 2018;18:e99–106. https://doi.org/10.1016/S1473-3099(17)30485-1.

[13] Grundmann H, Klugman KP, Walsh T, Ramon-Pardo P, Sigauque B, Khan W, et al. A framework for global surveillance of antibiotic resistance. Drug Resist Updat 2011;14:79–87. https://doi.org/10.1016/j.drup.2011.02.007.

[14] Centers for Disease Control and Prevention. Healthcare-Associated Infections - Community Interface Surveillance Report, Emerging Infections Program Network, Methicillin-Resistant Staphylococcus aureus, 2017. 2020. https://www.cdc.gov/hai/eip/pdf/2017-MRSA-Report-508.pdf (accessed December 13, 2021)

[15] Wertheim HFL, Vos MC, Ott A, van Belkum A, Voss A, Kluytmans JAJW, et al. Risk and outcome of nosocomial Staphylococcus aureus bacteraemia in nasal carriers versus non-carriers. Lancet 2004;364:703–5. https://doi.org/10.1016/S0140-6736(04)16897-9.

[16] von Eiff C, Becker K, Machka K, Stammer H, Peters G. Nasal Carriage as a Source of Staphylococcus aureus Bacteremia. N Engl J Med 2001;344:11–6. https://doi.org/10.1056/NEJM200101043440102.

[17] Centers for Disease Control and Prevention. National Healthcare Safety Network: Patient Safety Component 2021. https://www.cdc.gov/nhsn/psc/index.html (accessed June 23, 2021).

[18] Grundmann H, Schouls LM, Aanensen DM, Pluister GN, Tami A, Chlebowicz M, et al. The dynamic changes of dominant clones of Staphylococcus aureus causing bloodstream infections in the European region: Results of a second structured survey. Eurosurveillance 2014;19:20987. https://doi.org/10.2807/1560-7917.ES2014.19.49.20987.

[19] Global antimicrobial resistance surveillance system (GLASS) report: early implementation 2020. Geneva: World Health Organization; 2020. Licence: CC BY-NC-SA 3.0 IGO

[20] Emerging antimicrobial resistance reporting framework. Geneva: World Health Organization; 2018. Licence: CC BY-NC-SA 3.0 IGO.

Figure captions

Figure 1. Overview of participating surveillance programmes

Representatives of MRSA surveillance programmes were identified through the network of the ISAC MRSA working group (ISAC MRSA-WG) or through the participation in the European Antimicrobial Resistance Surveillance Network (EARS-Net). Listed are the numbers of contacted organisations and respective number of countries. Also listed are the number of returned surveys and presentations given at the webinar, for the respective number of included countries and surveillance programmes.

Figure 2. Proposal for harmonised MRSA surveillance

To harmonise surveillance, we propose (1) inclusion of all bloodstream infection (BSI) isolates and a representative sample of skin and soft-tissue infection (SSTI) isolates in proportion to MRSA prevalence, (2) integration of microbiological and epidemiological data in a single database using standardised report templates, and (3) implementation of central biobanks for collection and further characterisation of MRSA isolates. Orange flags depict the main challenges in harmonised surveillance.